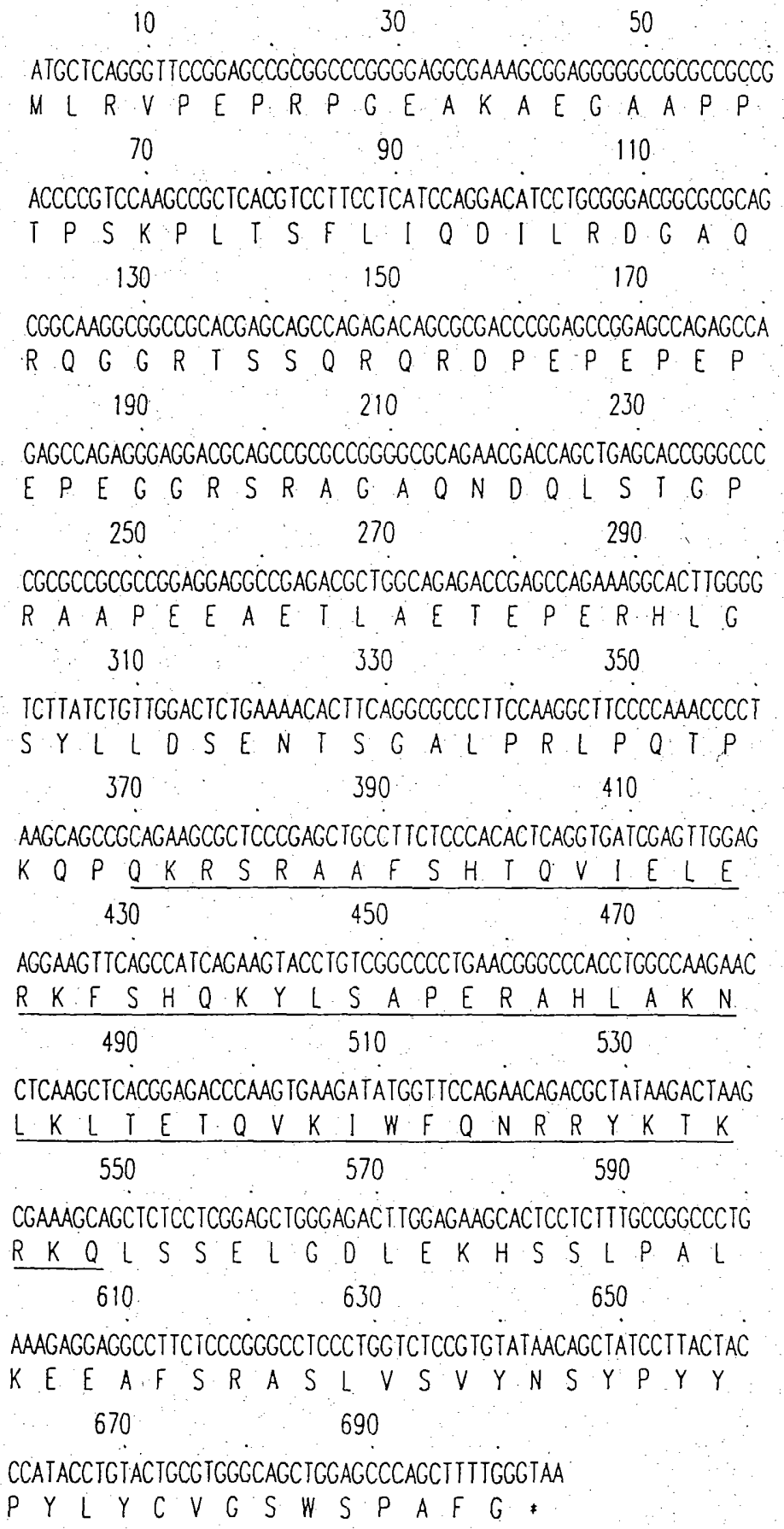
10 30 50
ATGCTCAGGGTTCCGGAGCCGCGGCCCCGGGGAGGCGAAAGCGGAGGGGGCCGCGCCGCCG
M L R V P E P R P G E A K A E G A A P P
70 90 110
ACCCCGTCCAAGCCGCTCACGTCCTTCCTCATCCAGGACATCCTGCGGGACGGCGCGCAG
T P S K P L T S F L I Q D I L R D G A Q
130 150 170
CGGCAAGGCGGCCGCACGAGCAGCCAGAGACAGCGCGACCCGGAGCCGGAGCCAGAGCCA
R Q G G R T S S Q R Q R D P E P E P E P
190 210 230
GAGCCAGAGGGAGGACGCAGCCGCGCCGGGGCGCAGAACGACCAGCTGAGCACCGGGCCC
E P E G G R S R A G A Q N D Q L S T G P
250 270 290
CGCGCCGCGCCGGAGGAGGCCGAGACGCTGGCAGAGACCGAGCCAGAAAGGCACTTGGGG
R A A P E E A E T L A E T E P E R H L G
310 330 350
TCTTATCTGTTGGACTCTGAAAACACTTCAGGCGCCCTTCCAAGGCTTCCCCAAACCCCT
S Y L L D S E N T S G A L P R L P Q T P
370 390 410
AAGCAGCCGCAGAAGCGCTCCCGAGCTGCCTTCTCCCACACTCAGGTGATCGAGTTGGAG
K Q P Q K R S R A A F S H T Q V I E L E
430 450 470
AGGAAGTTCAGCCATCAGAAGTACCTGTCGGCCCCTGAACGGGCCCACCTGGCCAAGAAC
R K F S H Q K Y L S A P E R A H L A K N
490 510 530
CTCAAGCTCACGGAGACCCAAGTGAAGATATGGTTCCAGAACAGACGCTATAAGACTAAG
L K L T E T Q V K I W F Q N R R Y K T K
550 570 590
CGAAAGCAGCTCTCCTCGGAGCTGGGAGACTTGGAGAAGCACTCCTCTTTGCCGGCCCTG
R K Q L S S E L G D L E K H S S L P A L
610 630 650
AAAGAGGAGGCCTTCTCCCGGGCCTCCCTGGTCTCCGTGTATAACAGCTATCCTTACTAC
K E E A F S R A S L V S V Y N S Y P Y Y
670 690
CCATACCTGTACTGCGTGGGCAGCTGGAGCCCAGCTTTTGGGTAA
P Y L Y C V G S W S P A F G *

FIG.1

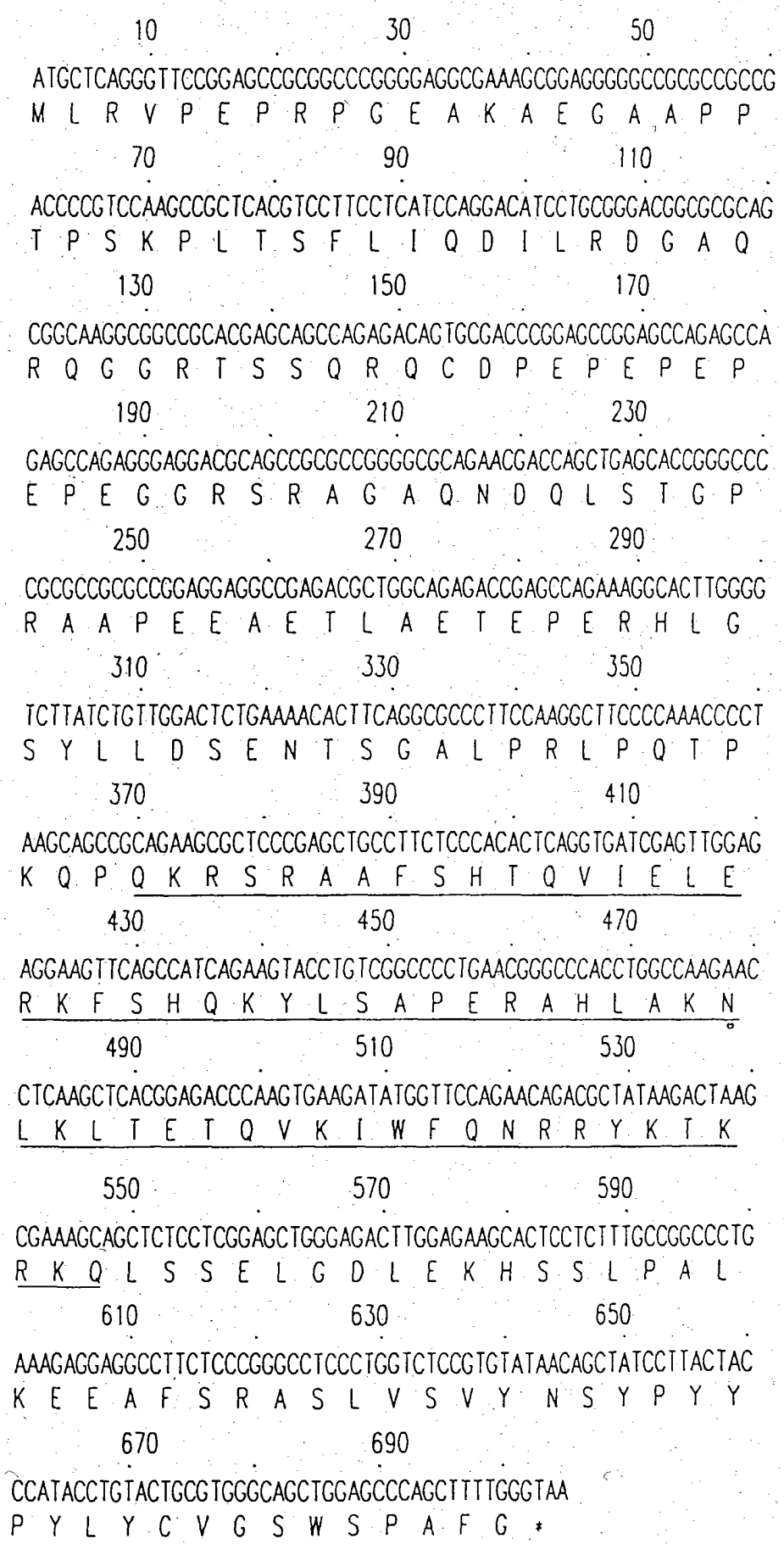
10 30 50
ATGCTCAGGGTTCCGGAGCCGCGGCCCGGGGAGGCGAAAGCGGAGGGGGCCGCGCCGCCG
M L R V P E P R P G E A K A E G A A P P
70 90 110
ACCCCGTCCAAGCCGCTCACGTCCTTCCTCATCCAGGACATCCTGCGGGACGGCGCGCAG
T P S K P L T S F L I Q D I L R D G A Q
130 150 170
CGGCAAGGCGGCCGCACGAGCAGCCAGAGACAGTGCGACCCGGAGCCGGAGCCAGAGCCA
R Q G G R T S S Q R Q C D P E P E P E P
190 210 230
GAGCCAGAGGGAGGACGCAGCCGCGCCGGGGCGCAGAACGACCAGCTGAGCACCGGGCCC
E P E G G R S R A G A Q N D Q L S T G P
250 270 290
CGCGCCGCGCCCGGAGGAGGCCGAGACGCTGGCAGAGACCGAGCCAGAAAGGCACTTGGGG
R A A P E E A E T L A E T E P E R H L G
310 330 350
TCTTATCTGTTGGACTCTGAAAACACTTCAGGCGCCCTTCCAAGGCTTCCCCAAACCCCT
S Y L L D S E N T S G A L P R L P Q T P
370 390 410
AAGCAGCCGCAGAAGCGCTCCCGAGCTGCCTTCTCCCACACTCAGGTGATCGAGTTGGAG
K Q P Q K R S R A A F S H T Q V I E L E
430 450 470
AGGAAGTTCAGCCATCAGAAGTACCTGTCGGCCCCTGAACGGGCCCACCTGGCCAAGAAC
R K F S H Q K Y L S A P E R A H L A K N
490 510 530
CTCAAGCTCACGGAGACCCAAGTGAAGATATGGTTCCAGAACAGACGCTATAAGACTAAG
L K L T E T Q V K I W F Q N R R Y K T K
550 570 590
CGAAAGCAGCTCTCCTCGGAGCTGGGAGACTTGGAGAAGCACTCCTCTTTGCCGGCCCTG
R K Q L S S E L G D L E K H S S L P A L
610 630 650
AAAGAGGAGGCCTTCTCCCGGGCCTCCCTGGTCTCCGTGTATAACAGCTATCCTTACTAC
K E E A F S R A S L V S V Y N S Y P Y Y
670 690
CCATACCTGTACTGCGTGGGCAGCTGGAGCCCAGCTTTTGGGTAA
P Y L Y C V G S W S P A F G *

FIG.2

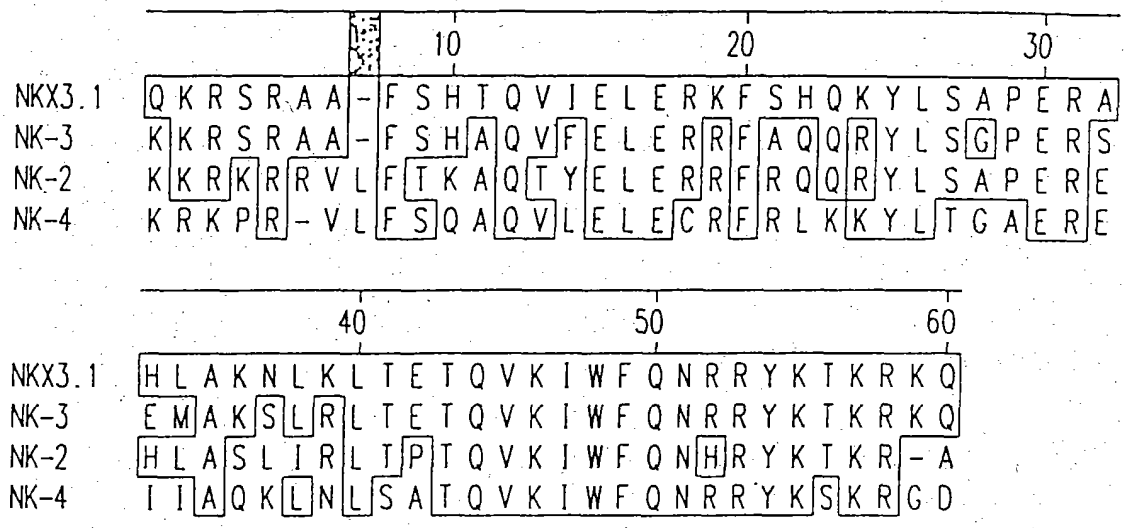
10
20
30
NKX3.1 Q K R S R A A - F S H T Q V I E L E R K F S H Q K Y L S A P E R A
NK-3 K K R S R A A - F S H A Q V F E L E R R F A Q Q R Y L S G P E R S
NK-2 K K R K R R V L F T K A Q T Y E L E R R F R Q Q R Y L S A P E R E
NK-4 K R K P R - V L F S Q A Q V L E L E C R F R L K K Y L T G A E R E
40
50
60
NKX3.1 H L A K N L K L T E T Q V K I W F Q N R R Y K T K R K Q
NK-3 E M A K S L R L T E T Q V K I W F Q N R R Y K T K R K Q
NK-2 H L A S L I R L T P T Q V K I W F Q N H R Y K T K R - A
NK-4 I I A Q K L N L S A T Q V K I W F Q N R R Y K S K R G D

FIG. 3A

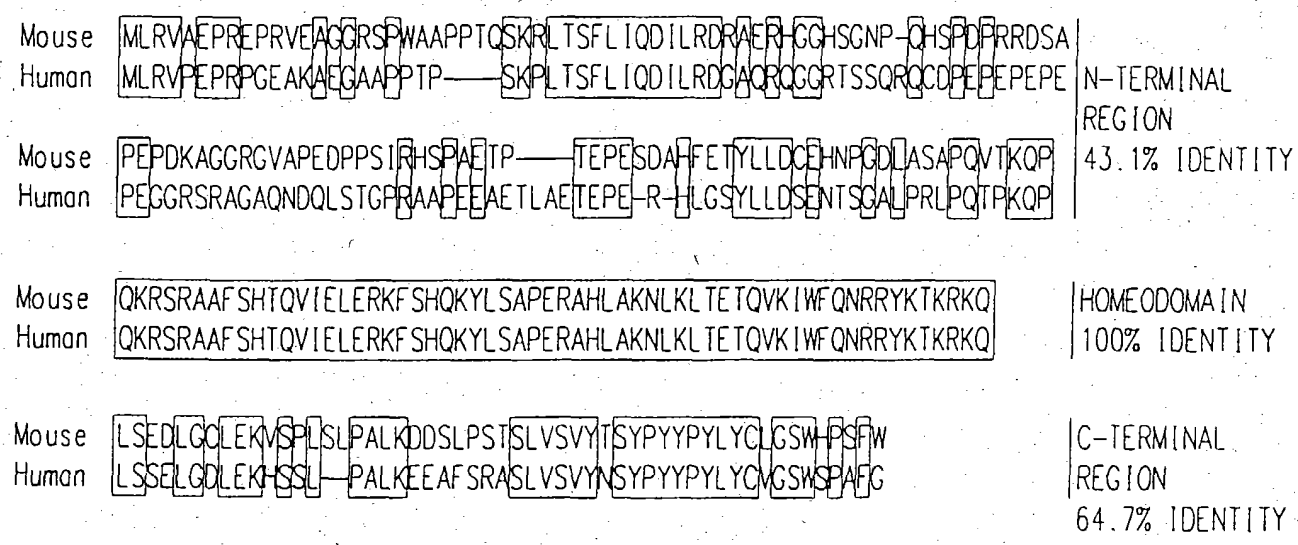
Mouse MLRVAEPREPRVEAGGRSPWAAPPTQSKRLTSFLIQDILRDRAERHGGHSGNP-QHSPDPRRDSA
Human MLRVPEPRPGEAKAEGAAPPTP——SKPLTSFLIQDILRDGAQRQGGRTSSQRQCDPEPEPEPE
N-TERMINAL REGION
43.1% IDENTITY
Mouse PEPDKAGGRGVAPEDPPSIRHSPAETP——TEPESDAFFETYLLDCEHNPGDLASAPQVTKQP
Human PEGGRSRAGAQNDQLSTGPRAAPEEAETLAETEPE-R-HLGSYLLDSENTSGALPRLPQTPKQP
Mouse QKRSRAAFSHTQVIELERKFSHQKYLSAPERAHLAKNLKLTETQVKIWFQNRRYKTKRKQ
Human QKRSRAAFSHTQVIELERKFSHQKYLSAPERAHLAKNLKLTETQVKIWFQNRRYKTKRKQ
HOMEODOMAIN
100% IDENTITY
Mouse LSEDLGDLEKVSPLSLPALKDDSLPSTSLVSVYTSYPYYPYLYCLGSWHPSFW
Human LSSELGDLEKHSSL—PALKEEAFSRASLVSVYNSYPYYPYLYCVGSWSPAFG
C-TERMINAL REGION
64.7% IDENTITY

FIG. 3B

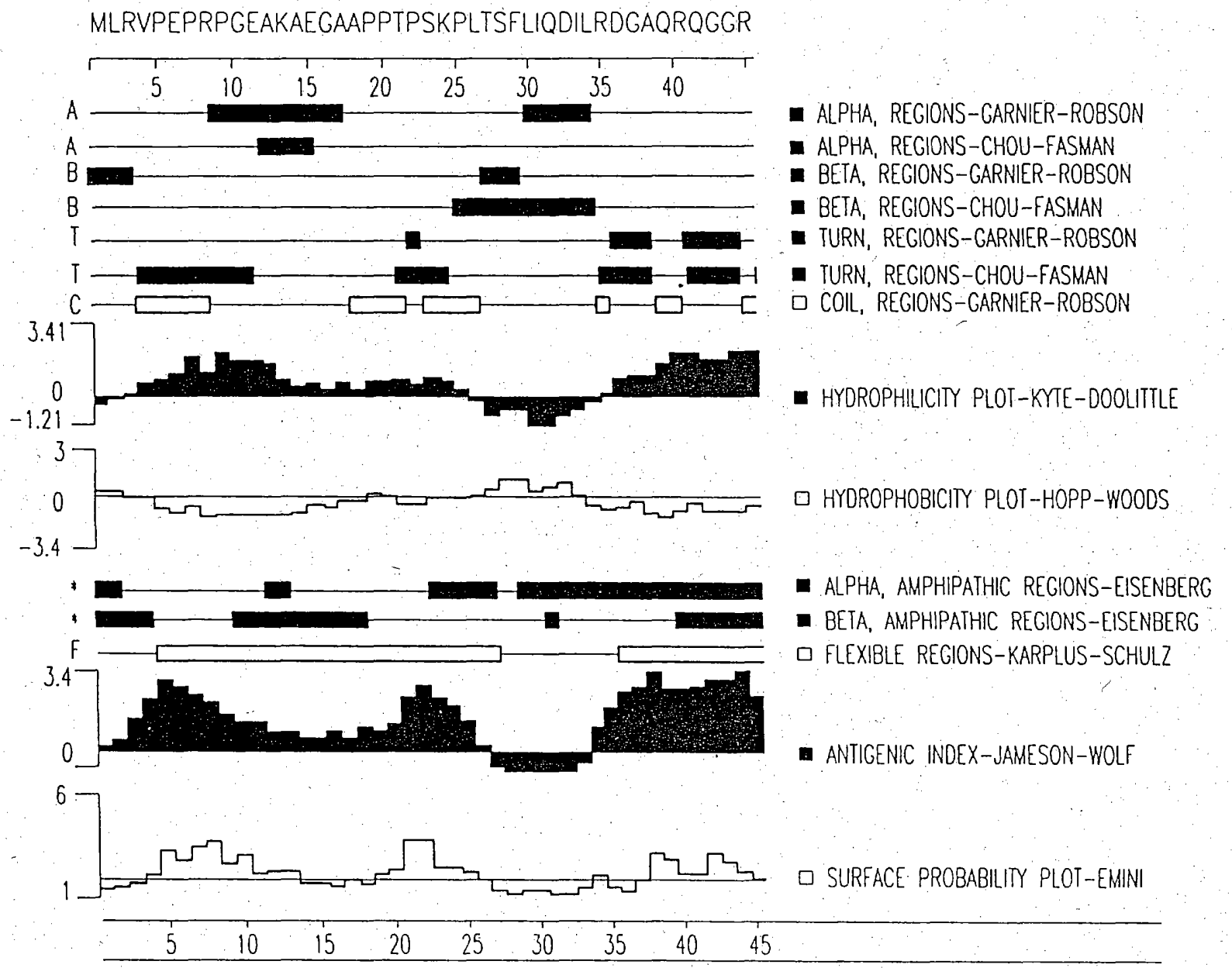
MLRVPEPRPGEAKAEGAAPPTPSKPLTSFLIQDILRDGAQRQGGR
5 10 15 20 25 30 35 40
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
3.41
0
-1.21
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
F
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
5 10 15 20 25 30 35 40 45

FIG.4A

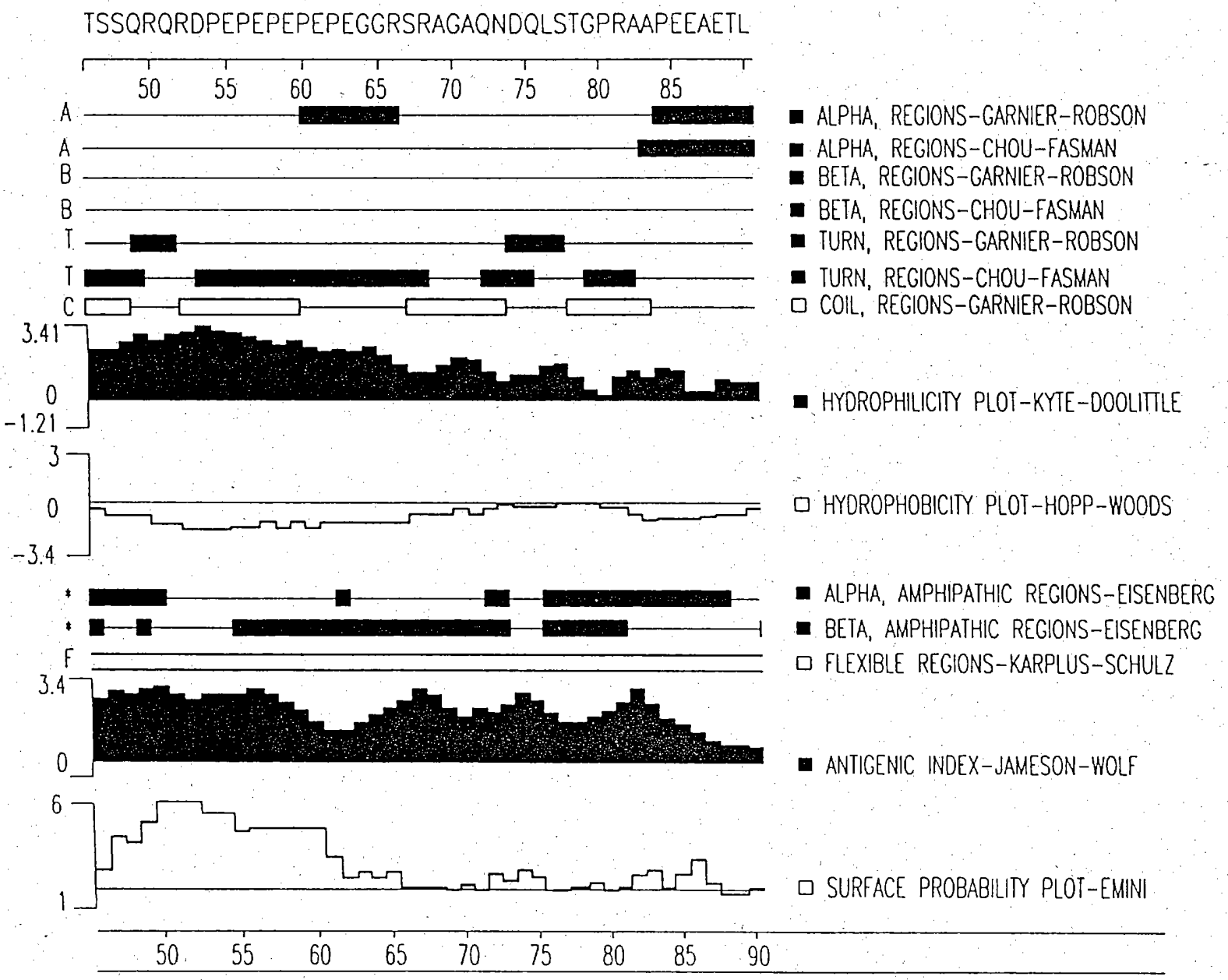
TSSQRQRDPEPEPEPEPEGGRSRAGAQNDQLSTGPRAAPEEAETL
50
55
60
65
70
75
80
85
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
3.41
0
-1.21
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
50
55
60
65
70
75
80
85
90

FIG. 4B

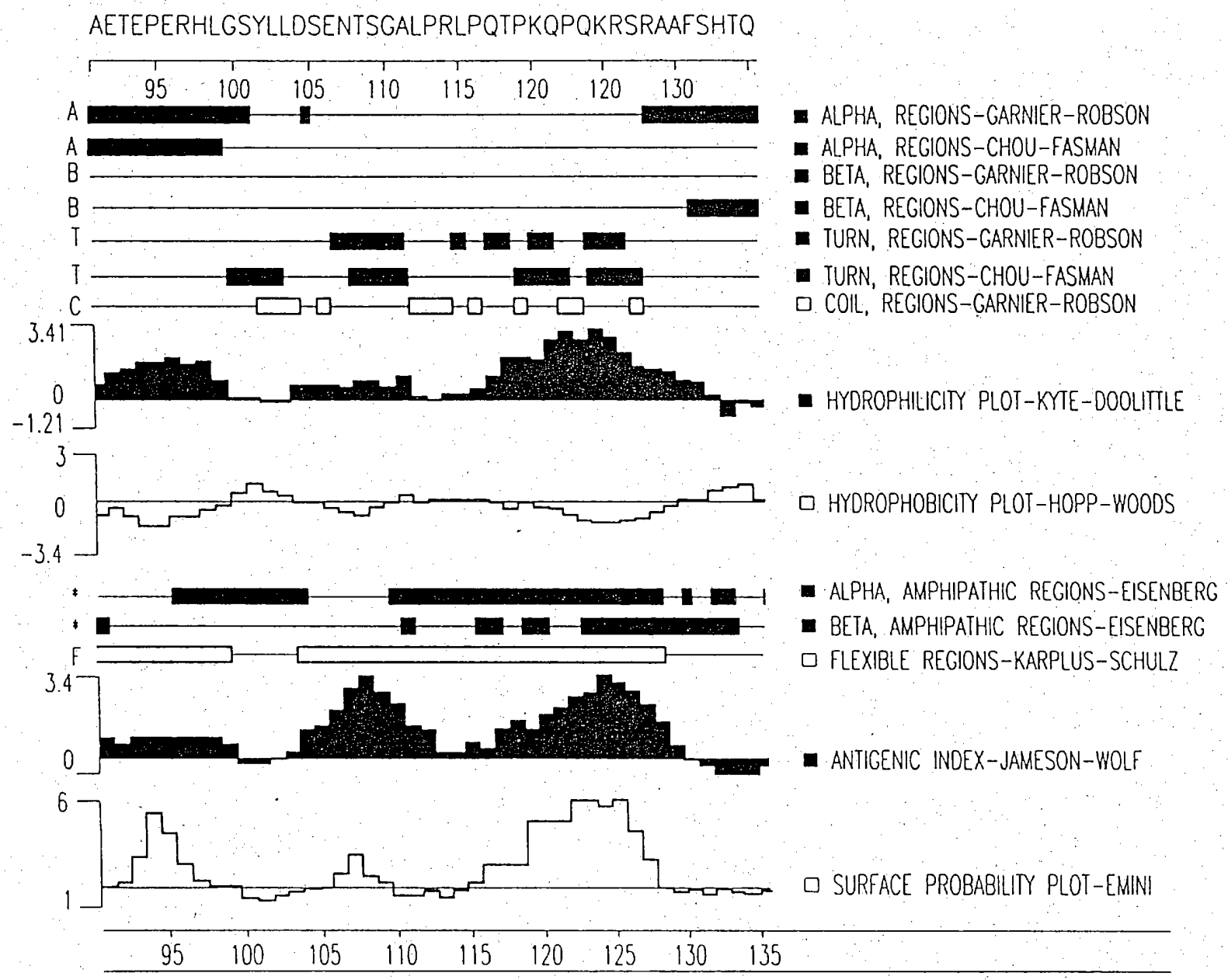
AETEPERHLGSYLLDSENTSGALPRLPQTPKQPQKRSRAAFSHTQ
95 100 105 110 115 120 120 130
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
3.41
0
-1.21
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
95 100 105 110 115 120 125 130 135

FIG. 4C

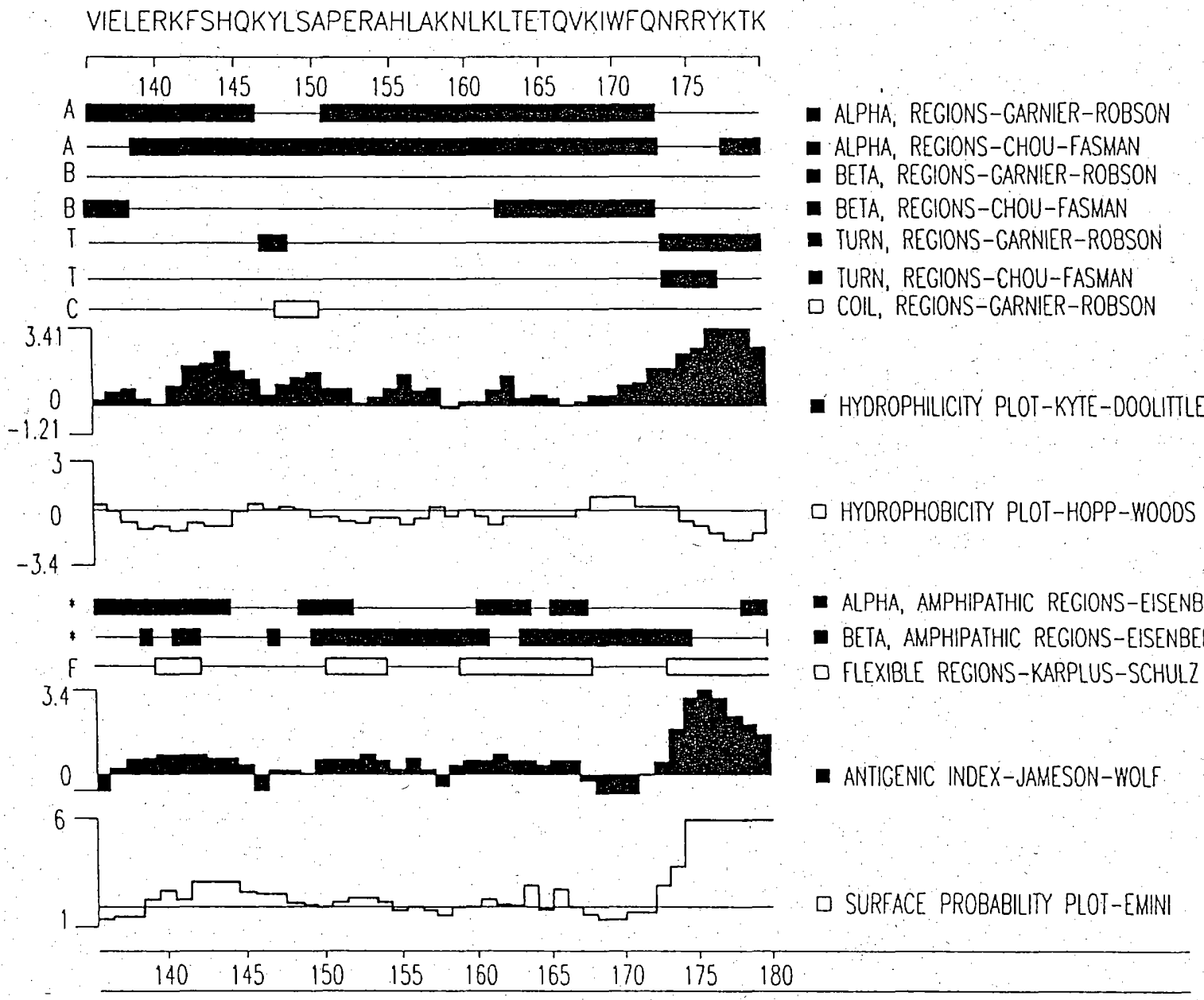
VIELERKFSHQKYLSAPERAHLAKNLKLTETQVKIWFQNRRYKTK
140 145 150 155 160 165 170 175
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
3.41
0
-1.21
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
140 145 150 155 160 165 170 175 180

FIG. 4D

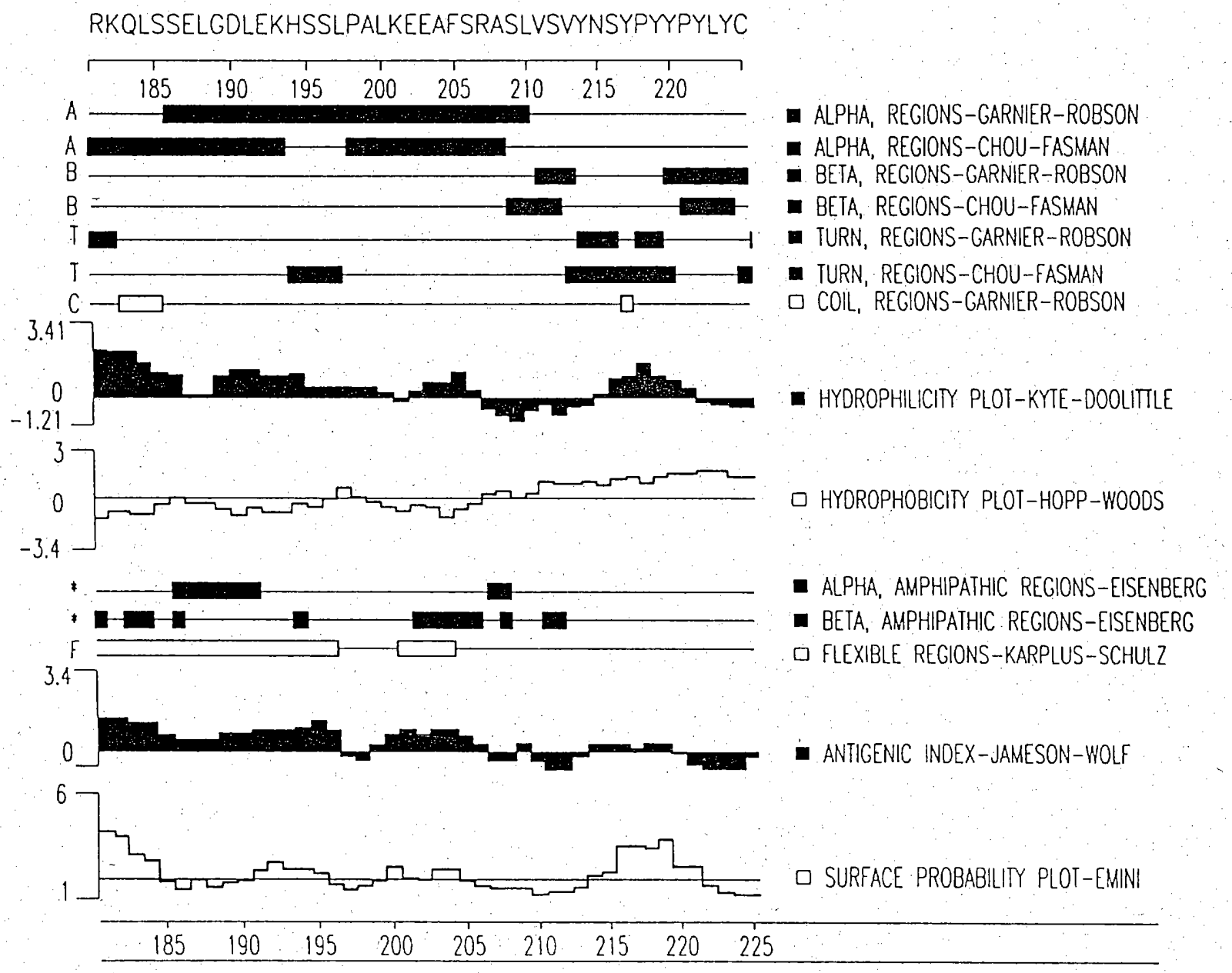
RKQLSSELGDLEKHSSLPALKEEAFSRASLVSVYNSYPYYPYLYC
185 190 195 200 205 210 215 220
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
3.41
0
-1.21
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
185 190 195 200 205 210 215 220 225

FIG. 4E

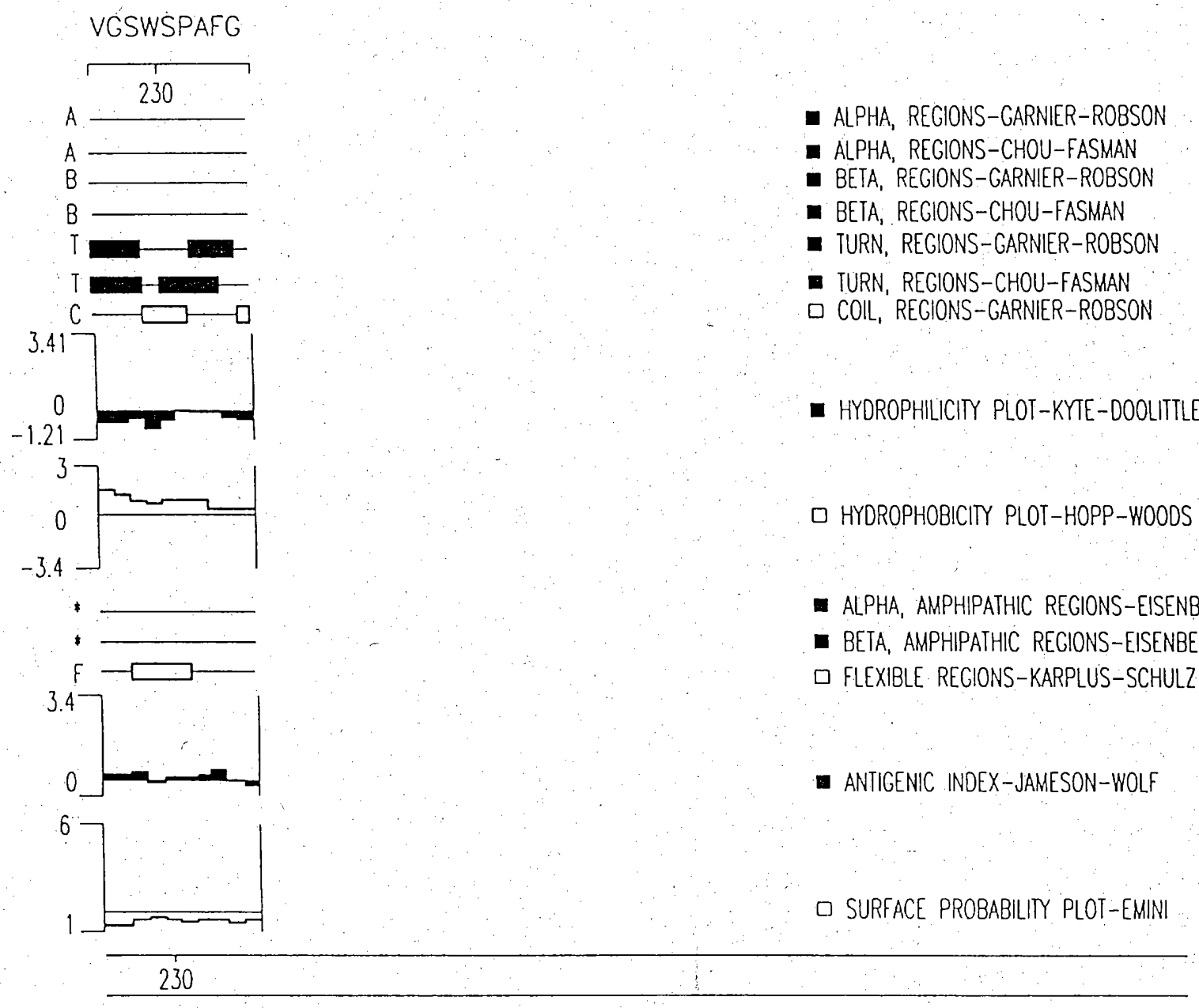
VGSWSPAFG
230
A
A
B
B
T
T
C
3.41
0
-1.21
3
0
-3.4
*
*
F
3.4
0
6
1
230
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG. 4F

```
1     AATTAACCCT CACTAAAGGG AACAAAAGCT GGAGCTCCAC
41    CGCGGTGGCG GCCGCGTAAT ACGACTCACT ATAGGGCGAA
81    GAATTCGGAT CTATCAATCT GCATCCTTGT TTCAGAACCA
121   TTTGATGTAA GTTTCATAAA TCTTGTGCCT TTGCTCCTAC
161   TTACTTCAGT GTTTATTTCC TAAAAATATT CTCTTGTACA
201   CTGACAGTAC AATGTGCAAT TTCAGTAAAT TTAACATTAA
241   TTCAATACTT CCATCATCGA CCTGACACTG AGACTCATGC
281   CTGTAGTCCT GGCACTTTGA GAGGCCAAGG CAGGAGGATC
321   ACTTGAATCC AGGAAATCGA GGCTGCAGTG AGTTATGATG
361   GCATCACTGC ACTCCAGCCT GGGCGGCAGA GGGAGACCCT
401   GTCCGTAAAA AACAGAAGAG AAAAGACAAG GAAAGAAAAT
441   ACTTCCATCA TCTCTGTTCC ACTTTCGTCT GTTGTCACGG
481   TACCGTCCAG TCCAGTCACA GTACCGGTTG GACCAATCTG
521   GCTAACCCAT TGTTTAGCCA ATGGGTTACA TGTTAACAGT
561   TGGTAATCTG CAAAAAGAGT ATGCTGATGT TCTTTTGAAC
601   TACTTTTTTA AATGCAGTTT TTGCATTTGT CCCTGGCCTA
641   AAACGCCTTC CATCCGTCTG GAAACTTTTC AAAAGGATGG
681   TATGTCATGT GTCTGGGGAG GAAGGAAAGT TAACAGGTTA
721   TTGCGGATAA AGGAACCACC AAAGAAAACC ACTTCTGCAA
761   CGGGAAAAGG CTTTGGCAAA GGTGTTTTCC TTCTTTCAGC
801   CTGGGGTCTG GCTGCACCTA CTTGTCATGC CTCTTTGAGG
841   TCGTAGATAT TGCAGATCTG AGTTTGCACC ATCTCTCCCA
881   GAGAGAGAGA GCACCCAGAA CTCTCACGGT ACCGCGCGGC
921   TGCAGTGACT GCGTGCTCAT CCCCTGTAAT TGGCTCTGAC
961   GGTCCTGAAG AGCTAACTGG ACTGTTTGTC TTGATCGTCC
1001  CATCCCCAGG AGCTTCTCTC TGCTGCGGGT GGGTTGGGGC
1041  AGAGGAGCCC CGCTTTGGGG TGCGCTCCTG GCCTGGGAAA
1081  ACGGCTCAGG GCGGAGGGAG GAGAGCTGGA GAAGGAGAGG
1121  AAATTGGGGA AGGAGAGGGA ATTGGGGAAG GAGAGGGAAC
1161  TGGGGAAGGA ATCCCCTAGG GAGGAGCGGA GCGGGGCAGT
1201  GCTCAGGGCT CGCAGATCGG CGGGGTCACC TGGGGCTCAG
1241  GGCGGCCAAT CCGCGGCGCG GCCCGTCCCG CGGCCAATGG
1281  GAGGGCGGCG CGGCCCGCTC CCCTGGGCTA TAAGCGAGCC
1321  GGGAGGCGGA AAGTGAAAGC GGTGCGGGCC GGGCGGGTGC
1361  ATTCAGGCCA AGGCGGGGCC GCCGGGATGC TCAGGGTTCC
1401  GGAGCCGCGG CCCGGGGAGG CGAAAGCGGA GGGGGCCGCG
1441  CCGCCGACCC CGTCCAAGCC GCTCACGTCC TTCCTCATCC
1481  AGGACATCCT GCGGGACGGC GCGCAGCGGC AAGGCGGCCG
1521  CACGAGCAGC CAGAGACAGC GCGACCCGGA GCCGGAGCCA
1561  GAGCCAGAGC CAGAGGGAGG ACGCAGCCGC GCCGGGGCGC
```

FIG. 5A

1601 AGAACGACCA GCTGAGCACC GGGCCCCGCG CCGCGCCGGA
1641 GGAGGCCGAG ACGCTGGCAG AGACCGAGCC AGGTAAGCGG
1681 CGAGGCCGGG GAAGGGGGGC AGCCCAAGGC GGACCCCCAG
1721 AGCTCGGGGT GCAGGGACGC GGGGCTCCGC GGCGACAGGC
1761 AGAGGGACCT TCCCGCCTCC GCAGCCACGC GCGCGCCCCC
1801 GGAATGAACC CTGAGCCCCA GCGTCAGGGC GGCGCAGGAT
1841 TCTGACACCG CAGGATTCGC CCGGTTCCGT GCCTTCCGTT
1881 CCCTGGGGCT CAGAAGCCGG CGCGACTGCA GCGCCACCGC
1921 CTTCCACCGT CCCAGGAGCG GATCCCGCCC CGCGCCACCC
1961 GCGATCGGCG CCAGCCCCCC GGTAGTTATG AGAANTAATA
2001 ATAACTTATT AACAGTGACA AAGCAGGGGT TGACCAGCAA
2041 AGCCTCCGTG TGCTTCCCAA TCCCGTGGGC AGTAAAGCGG
2081 TATATTCGGG GTTCCCTCCG GTGTCCAGGA GAGAGAGTCC
2121 ACTTATTTTC TTTCCTGTCA CTTCTGATGA GGCGACCGAA
2161 CGCCTCGTTT AGCGAAGAGG GAATTAAAGC CCAGAATGAG
2201 CCTGCCTCTG CGTCTCCAGT GGCACAAGCC CTCTCTTGCC
2241 CACCTGGATC CTAACACCGG ATGTCTTTTG GTCTGGCCTT
2281 CCCGGGTATC TTGTTCCACG GCATTTTCCC TGCCTCCCTC
2321 TCCCGCCTCT CCTCAGCACA CAGATCCAGA ATCCCCATAT
2361 AATTCTACTA GACAGTAGGG AGAAAGTTCA ACCACGAAAC
2401 GTCTCTAACT TTGGGTTCTT GATGATTCTT AGCAAATGAA
2441 TGCGTAATAA ACATATTTAC TCACTCTTCA CTCCGGAGAG
2481 CTCCTTAGTC ATGTGAAAAA AGTGAAATGT ATCCACGATG
2521 ACAGTGGGCT GTTTGTTCAC TCACTAAAGA GATAAGGGTG
2561 GATTGAATTC TCTTCTCTTC CCTGCTAACA TGTAACTTTT
2601 GTCTTCCCAT CCCTCCTTCC CCACTCTCCT TTCCAGAAAG
2641 GCACTTGGGG TCTTATCTGT TGGACTCTGA AAACACTTCA
2681 GGCGCCCTTC CAAGGCTTCC CCAAACCCCT AAGCAGCCGC
2721 AGAAGCGCTC CCGAGCTGCC TTCTCCCACA CTCAGGTGAT
2761 CGAGTTGGAG AGGAAGTTCA GCCATCAGAA GTACCTGTCG
2801 GCCCCTGAAC GGGCCCACCT GGCCAAGAAC CTCAAGCTCA
2841 CGGAGACCCA AGTGAAGATA TGGTTCCAGA ACAGACGCTA
2881 TAAGACTAAG CGAAAGCAGC TCTCCTCGGA GCTGGGAGAC
2921 TTGGAGAAGC ACTCCTCTTT GCCGGCCCTG AAAGAGGAGG
2961 CCTTCTCCCG GGCCTCCCTG GTCTCCGTGT ATAACAGCTA
3001 TCCTTACTAC CCATACCTGT ACTGCGTGGG CAGCTGGAGC
3041 CCAGCTTTTG GGTAATGCCA GCTCAGGTGA CAACCATTAT
3081 GATCAAAAAC TGCCTTCCCC AGGGTGTCTC TATGAAAAGC
3121 ACAAGGGGCC AAGGTCAGGG AGCAAGAGGT GTGCACACCA
3161 AAGCTATTGG AGATTTGCGT GGAAATCTCA GATTCTTCAC

FIG. 5B

3201 TGGTGAGACA ATGAAACAAC AGAGACAGTG AAAGTTTTAA
3241 TACCTAAGTC ATTCCTCCAG TGCATACTGT AGGTCATTTT
3281 TTTTGGTTCT GGCTACCTGT TTGAAGGGGA GAGAGGGAAA
3321 ATCAAGTGGT ATTTTCCAGC ACTTTGTATG ATTTTGGATG
3361 AGTTGTACAC CCAAGGATTC TGTTATGCAA CTCCATCCTC
3401 CTGTGTCACT GAATATCAAC TCTGAAAGAG CAAACCTAAC
3441 AGGAGAAAGG ACAACCAGGA TGAGGATGTC ACCAACTGAA
3481 TTAAACTC

FIG. 5C

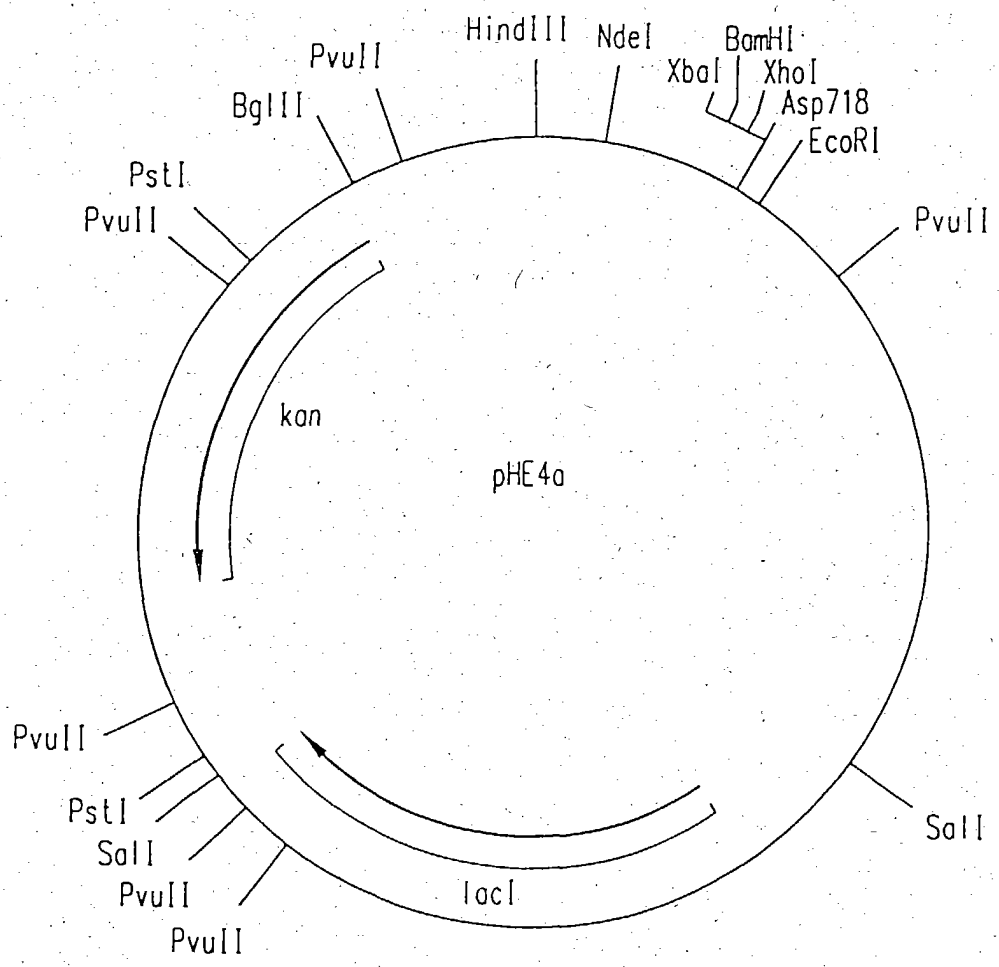

FIG. 6

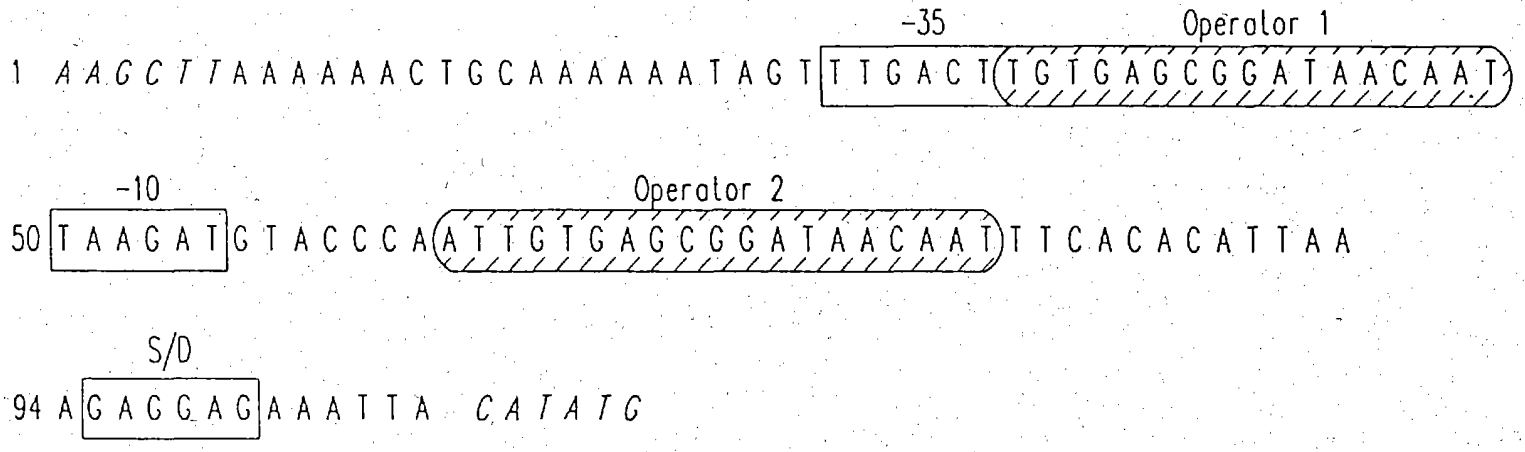
-35
Operator 1
1 AAGCTTAAAAAACTGCAAAAAATAGTTTGACTTGTGAGCGGATAACAAT
-10
Operator 2
50 TAAGATGTACCCAATTGTGAGCGGATAACAATTTCACACATTAA
S/D
94 AGAGGAGAAATTA CATATG

FIG.7